

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/768,886A
Source: IFW/6
Date Processed by STIC: 6/2/06

ENTERED



IFW16

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/768,886A

DATE: 06/02/2006

TIME: 09:48:18

Input Set : A:\MAPK5.(Supp).txt
 Output Set: N:\CRF4\06022006\J768886A.raw

3 <110> APPLICANT: Board of Trustees for University of Arkansas
 5 <120> TITLE OF INVENTION: Mitogen-Activated Protein Kinase and Method of Use to
 Enhance
 6 Biotic and Abiotic Stress Tolerance in Plants
 8 <130> FILE REFERENCE: UAF-03-14
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/768,886A
 11 <141> CURRENT FILING DATE: 2004-01-31
 13 <160> NUMBER OF SEQ ID NOS: 10
 15 <170> SOFTWARE: PatentIn version 3.2
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 1396
 19 <212> TYPE: DNA
 20 <213> ORGANISM: Oryza sativa
 22 <400> SEQUENCE: 1
 23 agagagtctgataatttaggttggtcaattcg gctgcttgcg gcgagagaag 60
 25 aggaggaggatttaggatg gacggggcgc cggtgccgaa gttcaggccg acgtgacgc 120
 27 acggcggccg gtacctgctc tacgacatct tcggaaacaa ttgcggatgtt acgaacaagt 180
 29 accagccgccc catcatgccc attggcccg ggcgcctacgg gatcgtctgc tccgtgatga 240
 31 actttgagac gagggagatg gtggcgatcaa agaagatcgc caacgcgttc aacaacgaca 300
 33 tggacgccaa ggcacgcgc cgggagatca agtcctcag gcacccgtac cacgagaaca 360
 35 tcataggcat cagggatgtg atcccccccg cgatccctca ggcgttcaac gacgtctaca 420
 37 tcgcccacgga gtcatggac accgacctcc atcacatcat ccgctccaac caagaactgt 480
 39 cagaagagca ctgccagtat ttccctgtacc agatcctcgc ggggctcaag tacatccact 540
 41 cggcgaacgt gatccaccgc gacctaagc cgagcaaccc gtcgttcaac gccaactgcg 600
 43 acctaagat ctgcgacttc gggctggcg ggcgcgtc ggagagcgcg atgtgacgg 660
 45 agtacgttgt caccgcgtgg taccgcgcgc cggagctgt gtcacttcc accgactact 720
 47 cccgcgcatt cgacgtctgg tccgtcggt gcatcttcat ggagctcatc aaccgcgc 780
 49 cgcttctccc cggcaggggac cacatgcacc agatgcgcct catcaccgag gtgatcg 840
 51 cggcgcggca cgacgagctg ggggtcatac ggaacgagga cgcgaggaag tacatgaggc 900
 53 acctgcgcga gtaccgcgc cggacgttcg cgagcatgtt cccgcgggtg cagccgcgc 960
 55 cgctcgacct catcgagagg atgctcacct tcaacccgcg cagagaatc acagttgagg 1020
 57 aggcgctcga tcatccttac cttagagat tgacgcacat cgccgatgag cccatctgcc 1080
 59 tggagccctt ctccttcgac ttccggcaga aggctctaaa cgaggaccaa atgaagcgc 1140
 61 tgcatttcaa cgaagcgcgc gagatgaacc caaacatccg gtactatgat gaatcaccat 1200
 63 gggaaatgaga tcccgtctat acctgtttt tacatatgat caagatttag agccgggttag 1260
 65 actgaacatt gcatttttt gttgtttagt gttcgaaacc cacattctt gcaagttgtg 1320
 67 gtcgtttgt atgatatatg gtactatgtt cgaataaaag gttttggAAC tttggattaa 1380
 69 aaaaaaaaaaaaaaa 1396
 72 <210> SEQ ID NO: 2
 73 <211> LENGTH: 368
 74 <212> TYPE: PRT
 75 <213> ORGANISM: Oryza sativa
 77 <400> SEQUENCE: 2
 79 Met Asp Gly Ala Pro Val Ala Glu Phe Arg Pro Thr Met Thr His Gly

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80 1 5 10 15
 83 Gly Arg Tyr Leu Leu Tyr Asp Ile Phe Gly Asn Lys Phe Glu Val Thr
 84 20 25 30
 87 Asn Lys Tyr Gln Pro Pro Ile Met Pro Ile Gly Arg Gly Ala Tyr Gly
 88 35 40 45
 91 Ile Val Cys Ser Val Met Asn Phe Glu Thr Arg Glu Met Val Ala Ile
 92 50 55 60
 95 Lys Lys Ile Ala Asn Ala Phe Asn Asn Asp Met Asp Ala Lys Arg Thr
 96 65 70 75 80
 99 Leu Arg Glu Ile Lys Leu Leu Arg His Leu Asp His Glu Asn Ile Ile
 100 85 90 95
 103 Gly Ile Arg Asp Val Ile Pro Pro Ile Pro Gln Ala Phe Asn Asp
 104 100 105 110
 107 Val Tyr Ile Ala Thr Glu Leu Met Asp Thr Asp Leu His His Ile Ile
 108 115 120 125
 111 Arg Ser Asn Gln Glu Leu Ser Glu Glu His Cys Gln Tyr Phe Leu Tyr
 112 130 135 140
 115 Gln Ile Leu Arg Gly Leu Lys Tyr Ile His Ser Ala Asn Val Ile His
 116 145 150 155 160
 119 Arg Asp Leu Lys Pro Ser Asn Leu Leu Leu Asn Ala Asn Cys Asp Leu
 120 165 170 175
 123 Lys Ile Cys Asp Phe Gly Leu Ala Arg Pro Ser Ser Glu Ser Asp Met
 124 180 185 190
 127 Met Thr Glu Tyr Val Val Thr Arg Trp Tyr Arg Ala Pro Glu Leu Leu
 128 195 200 205
 131 Leu Asn Ser Thr Asp Tyr Ser Ala Ala Asp Val Trp Ser Val Gly Cys
 132 210 215 220
 135 Ile Phe Met Glu Leu Ile Asn Arg Gln Pro Leu Phe Pro Gly Arg Asp
 136 225 230 235 240
 139 His Met His Gln Met Arg Leu Ile Thr Glu Val Ile Gly Thr Pro Thr
 140 245 250 255
 143 Asp Asp Glu Leu Gly Phe Ile Arg Asn Glu Asp Ala Arg Lys Tyr Met
 144 260 265 270
 147 Arg His Leu Pro Gln Tyr Pro Arg Arg Thr Phe Ala Ser Met Phe Pro
 148 275 280 285
 151 Arg Val Gln Pro Ala Ala Leu Asp Leu Ile Glu Arg Met Leu Thr Phe
 152 290 295 300
 155 Asn Pro Leu Gln Arg Ile Thr Val Glu Glu Ala Leu Asp His Pro Tyr
 156 305 310 315 320
 159 Leu Glu Arg Leu His Asp Ile Ala Asp Glu Pro Ile Cys Leu Glu Pro
 160 325 330 335
 163 Phe Ser Phe Asp Phe Glu Gln Lys Ala Leu Asn Glu Asp Gln Met Lys
 164 340 345 350
 167 Gln Leu Ile Phe Asn Glu Ala Ile Glu Met Asn Pro Asn Ile Arg Tyr
 168 355 360 365
 171 <210> SEQ ID NO: 3
 172 <211> LENGTH: 1084
 173 <212> TYPE: DNA
 174 <213> ORGANISM: Oryza sativa

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176 <400> SEQUENCE: 3
177 agagagtcag ataaggctgt taatttagttt ggtcaattcg gctgcttgcg gcgagagaag 60
179 aggaggaggg attaggatg gacggggcgc cggtggcga gttcaggccg acgatgacgc 120
181 acggcggccg gtacctgctc tacgacatct tcggaaacaa gttcgaggtg acgaacaagt 180
183 accagccgcc catcatgccc attggccgcg gcgcctacgg gatcgtctgc tccgtatga 240
185 actttgagac gagggagatg gtggcgataa agaagatcgc caactgcac ctcaagatct 300
187 gcgacttcgg gctggcgcgg cctgcgtcgg aqagcgacat gatgacggag tacgtggta 360
189 cccgggtgta ccgcgcgcg gagctgctgc tcaactccac cgactactcc gcccgcac 420
191 acgtctggtc cgtcggctgc atcttcatgg agctcatcaa cccgcagccg ctcttccccg 480
193 gcagggacc a catgaccagg atgcgcctca tcaccgaggt gatcgggacg cgcacggacg 540
195 acgagctggg gttcatacgg aacqaggacg cgaggaagta catgaggcac ctggcgcagt 600
197 acccgcgcgcg gacggttcgcg agcatgttcc cgccgggtgca gcccgcgcg ctgcacctca 660
199 tcgagaggat gtcacaccc aacccgctgc agagaatcac agttgaggag gcgcctgatc 720
201 atccttaccc agagagattt cacgacatcg ccgatgagcc catctgcctg gagcccttct 780
203 ctttcgactt cgagcagaag gctctaaacg aggaccaaattt gaagcagttt atcttcaacg 840
205 aagcgatcga gatgaaccca aacatccgg actagatttga atcaccatgg aaatgagatc 900
207 ccgtctatac ctgctttgtt catatgatca agattgagag ccgggttagac tgaacattgc 960
209 atttgtttgtt ttgtttagtgc tcgaaaccca cattctctgc aagttgtggc tgctttgttat 1020
211 gatatatggt actatgttcg aataaaaaggg tttggaaactt tggattaaaa aaaaaaaaaa 1080
213 aaaa 1084
216 <210> SEQ ID NO: 4
217 <211> LENGTH: 266
218 <212> TYPE: PRT
219 <213> ORGANISM: Oryza sativa
221 <400> SEQUENCE: 4
223 Met Met Asp Gly Ala Pro Val Ala Glu Phe Arg Pro Thr Met Thr His
224 1 5 10 15
227 Gly Gly Arg Tyr Leu Leu Tyr Asp Ile Phe Gly Asn Lys Phe Glu Val
228 20 25 30
231 Thr Asn Lys Tyr Gln Pro Pro Ile Met Pro Ile Gly Arg Gly Ala Tyr
232 35 40 45
235 Gly Ile Val Cys Ser Val Met Asn Phe Glu Thr Arg Glu Met Val Ala
236 50 55 60
239 Ile Lys Lys Ile Ala Asn Cys Asp Leu Lys Ile Cys Asp Phe Gly Leu
240 65 70 75 80
243 Ala Arg Pro Ser Ser Glu Ser Asp Met Met Thr Glu Tyr Val Val Thr
244 85 90 95
247 Arg Trp Tyr Arg Ala Pro Glu Leu Leu Asn Ser Thr Asp Tyr Ser
248 100 105 110
251 Ala Ala Ile Asp Val Trp Ser Val Gly Cys Ile Phe Met Glu Leu Ile
252 115 120 125
255 Asn Arg Gln Pro Leu Phe Pro Gly Arg Asp His Met His Gln Met Arg
256 130 135 140
259 Leu Ile Thr Glu Val Ile Gly Thr Pro Thr Asp Asp Glu Leu Gly Phe
260 145 150 155 160
263 Ile Arg Asn Glu Asp Ala Arg Lys Tyr Met Arg His Leu Pro Gln Tyr
264 165 170 175
267 Pro Arg Arg Thr Phe Ala Ser Met Phe Pro Arg Val Gln Pro Ala Ala
268 180 185 190

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271 Leu Asp Leu Ile Glu Arg Met Leu Thr Phe Asn Pro Leu Gln Arg Ile
 272 195 200 205
 275 Thr Val Glu Ala Leu Asp His Pro Tyr Leu Glu Arg Leu His Asp
 276 210 215 220
 279 Ile Ala Asp Glu Pro Ile Cys Leu Glu Pro Phe Ser Phe Asp Phe Glu
 280 225 230 235 240
 283 Gln Lys Ala Leu Asn Glu Asp Gln Met Lys Gln Leu Ile Phe Asp Glu
 284 245 250 255
 287 Ala Ile Glu Met Asn Pro Asn Ile Arg Tyr
 288 260 265
 291 <210> SEQ ID NO: 5
 292 <211> LENGTH: 26
 293 <212> TYPE: DNA
 294 <213> ORGANISM: Artificial
 296 <220> FEATURE:
 297 <223> OTHER INFORMATION: gene-specific primer containing restriction site
 299 <400> SEQUENCE: 5
 300 cgggatccgt cggtgcatt ttcattg 26
 303 <210> SEQ ID NO: 6
 304 <211> LENGTH: 25
 305 <212> TYPE: DNA
 306 <213> ORGANISM: Artificial
 308 <220> FEATURE:
 309 <223> OTHER INFORMATION: gene-specific primer containing restriction site
 311 <400> SEQUENCE: 6
 312 gctctagatt caatctagta ccggaa 25
 315 <210> SEQ ID NO: 7
 316 <211> LENGTH: 20
 317 <212> TYPE: DNA
 318 <213> ORGANISM: Artificial
 320 <220> FEATURE:
 321 <223> OTHER INFORMATION: gene-specific primer containing restriction site
 323 <400> SEQUENCE: 7
 324 gagttcaggc cgacgatgac 20
 327 <210> SEQ ID NO: 8
 328 <211> LENGTH: 20
 329 <212> TYPE: DNA
 330 <213> ORGANISM: Artificial
 332 <220> FEATURE:
 333 <223> OTHER INFORMATION: gene-specific primer containing restriction site
 335 <400> SEQUENCE: 8
 336 atcggcgatg tcgtgcaatc 20
 339 <210> SEQ ID NO: 9
 340 <211> LENGTH: 368
 341 <212> TYPE: PRT
 342 <213> ORGANISM: Triticum aestivum
 344 <400> SEQUENCE: 9
 346 Met Asp Gly Ala Pro Val Ala Glu Phe Arg Pro Thr Met Thr His Gly
 347 1 5 10 15

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350 Gly Arg Phe Leu Leu Tyr Asn Ile Phe Gly Asn Gln Phe Glu Thr Thr
 351 20 25 30
 354 Ala Lys Tyr Gln Pro Pro Ile Met Pro Ile Gly Lys Gly Ala Tyr Gly
 355 35 40 45
 358 Ile Val Cys Ser Val Met Asn Phe Glu Thr Arg Glu Met Val Ala Ser
 359 50 55 60
 362 Lys Lys Ile Ala Asn Ala Phe Asp Asn Asn Met Asp Ala Lys Arg Thr
 363 65 70 75 80
 366 Leu Arg Glu Ile Lys Leu Leu Leu Arg His Leu Asp Glu Asn Ile Val
 367 85 90 95
 370 Gly Leu Arg Asp Val Ile Pro Pro Ala Ile Pro Gln Ser Glu Asn Asp
 371 100 105 110
 374 Val Tyr Ile Ala Thr Glu Leu Met Asp Thr Asp Leu His His Ile Ile
 375 115 120 125
 378 Arg Ser Asn Gly Glu Leu Ser Glu Glu His Glu Gln Tyr Phe Leu Tyr
 379 130 135 140
 382 Gln Leu Leu Arg Gly Leu Lys Tyr Ile His Ser Ala Asn Val Ile His
 383 145 150 155 160
 386 Arg Asp Leu Lys Pro Ser Asn Leu Leu Leu Asn Ala Asn Cys Asp Leu
 387 165 170 175
 390 Lys Ile Cys Asp Phe Gly Leu Ala Arg Pro Ser Ser Glu Ser Asp Met
 391 180 185 190
 394 Met Thr Glu Tyr Val Val Thr Arg Trp Tyr Arg Ala Pro Glu Leu Leu
 395 195 200 205
 398 Leu Asn Ser Thr Asp Tyr Ser Ala Asn Ile Asp Val Trp Ser Val Gly
 399 210 215 220
 402 Cys Ile Phe Met Glu Leu Ile Asn Arg Ala Pro Leu Phe Pro Gly Arg
 403 225 230 235 240
 406 Asp His Met His Gln Met Arg Leu Ile Thr Glu Val Ile Gly Thr Pro
 407 245 250 255
 410 Thr Asp Asp Asp Leu Gly Phe Ile Arg Asn Glu Asp Ala Arg Arg Tyr
 411 260 265 270
 414 Met Arg His Leu Pro Gln Phe Pro Arg Arg Ser Phe Pro Gly Phe Pro
 415 275 280 285
 418 Lys Val Gln Pro Ala Ala Leu Asp Leu Ile Glu Arg Met Leu Thr Phe
 419 290 295 300
 422 Asn Pro Leu Gln Arg Ile Thr Val Glu Glu Ala Leu Glu His Pro Tyr
 423 305 310 315 320
 426 Leu Glu Arg Leu His Asp Val Ala Asp Glu Pro Ile Cys Thr Asp Pro
 427 325 330 335
 430 Phe Ser Phe Asp Phe Glu Gln His Pro Leu Thr Glu Asp Gln Met Lys
 431 340 345 350
 434 Leu Ile Pro Glu Asn Glu Ala Leu Glu Leu Asn Pro Asn Phe Arg Tyr
 435 355 360 365
 438 <210> SEQ ID NO: 10
 439 <211> LENGTH: 371
 440 <212> TYPE: PRT
 441 <213> ORGANISM: Nicotiana tabacum
 443 <400> SEQUENCE: 10

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 06/02/2006
PATENT APPLICATION: US/10/768,886A TIME: 09:48:19

Input Set : A:\MAPK5 (Supp).txt
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:5,6,7,8

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/768,886A

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Input Set : A:\MAPK5 (Supp).txt

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L:10 M:270 C: Current Application Number differs, Replaced Current Application Number